



# **STIC Search Report**

## **Biotech-Chem Library**

**STIC Database Tracking Number: 107969**

**TO: Terra Gibbs**  
**Location: CM1/12A12/11E12**  
**Art Unit: 1635**  
**Monday, November 10, 2003**

**Case Serial Number: 09/774809**

**From: David Schreiber**  
**Location: Biotech-Chem Library**  
**CM1-6A03**  
**Phone: 308-4292**

**david.schreiber@uspto.gov**

### **Search Notes**

Access DB# \_\_\_\_\_

**SEARCH REQUEST FORM**

Scientific and Technical Information Center

Requester's Full Name: \_\_\_\_\_ Examiner #: \_\_\_\_\_ Date: \_\_\_\_\_  
 Art Unit: \_\_\_\_\_ Phone Number 30 \_\_\_\_\_ Serial Number: \_\_\_\_\_  
 Mail Box and Bldg/Room Location: \_\_\_\_\_ Results Format Preferred (circle): PAPER DISK E-MAIL

If more than one search is submitted, please prioritize searches in order of need.

\*\*\*\*\*

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc. if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention: \_\_\_\_\_

Inventors (please provide full names): \_\_\_\_\_

Earliest Priority Filing Date: \_\_\_\_\_

*\*For Sequence Searches Only\* Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.*

**STAFF USE ONLY**

	Type of Search	Vendors and cost where applicable
Searcher <u>D. Schreiber</u>	NA Sequence (#) <u>6</u>	STN _____
Searcher Phone # <u>308-4292</u>	AA Sequence (#) _____	Dialog _____
Searcher Location <u>CML 6A03</u>	Structure (#) _____	Questel Orbit _____
Date Searcher Broken In _____	Bibliographic _____	Dr Link _____
Date Completed <u>11/10</u>	Litigation _____	Lexis Nexis _____
Searcher Prep & Review Time <u>20</u>	Fulltext _____	Sequence Systems <u>CompuGen</u>
Client Prep Time _____	Patent Family _____	WWW Internet _____
Online Time <u>102</u>	Other _____	Other (specify) _____

PTOL 596-112100

Schreiber, David

107969

From: Gibbs, Terra 79523  
Sent: Monday, November 03, 2003 11:31 AM  
To: Schreiber, David  
Subject: Sequence search request...

Hi David,

Doug Schultz and Karen LaCourcie recommended that I send you this search request.

I have a request for a score over length search:

I need a length limited nucleotide sequence search against SEQ ID NO:31 of USSN 09/774,809, where the returns are rank ordered based on the score over length/ratio as we've discussed. I need the lengths limited to hits between 8 and 30 nucleotides, and I'll take as many hits as you can import into excel (64,000?), and alignments for anything above .75 on the above ratio. Hope this is clear, please call me if it's not. I do not need the interference databases searched.

Thanks!

Terra Cotta Gibbs, Ph.D.

; Art Unit 1635

CM1, 12A12

703-306-3221

20  
3 p 6.6 3 h  
3 h 8.2  
21.1  
4  
51



# STIC SEARCH RESULTS FEEDBACK FORM

## Biotech-Chem Library

Questions about the scope or the results of the search? Contact *the searcher or contact*:

Mary Hale, Information Branch Supervisor  
308-4258, CM1-1E01

## Voluntary Results Feedback Form

➤ I am an examiner in Workgroup:  Example: 1610

➤ Relevant prior art **found**, search results used as follows:

- ☐ 102 rejection
- ☐ 103 rejection
- ☐ Cited as being of interest.
- ☐ Helped examiner better understand the invention.
- ☐ Helped examiner better understand the state of the art in their technology.

Types of relevant prior art found:

- ☐ Foreign Patent(s)
- ☐ Non-Patent Literature  
(journal articles, conference proceedings, new product announcements etc.)

➤ Relevant prior art **not found**:

- ☐ Results verified the lack of relevant prior art (helped determine patentability).
- ☐ Results were not useful in determining patentability or understanding the invention.

Comments:

Drop off or send completed forms to STIC/Biotech-Chem Library CM1 – Circ. Desk



GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: November 5, 2003, 03:41:20 ; Search time 1368 Seconds  
(without alignments)  
598.094 Million cell updates/sec

Title: US-09-774-809-31  
Perfect score: 20  
Sequence: 1 gtccgggccaggccaaagtc 20

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2888711 seqs, 20454813386 residues

Total number of hits satisfying chosen parameters: 1007914

Minimum DB seq length: 8  
Maximum DB seq length: 30

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 65000 summaries

Database : GenEmbl.\*

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- 2: gb\_htg.\*
- 3: gb\_in.\*
- 4: gb\_om.\*
- 5: gb\_ov.\*
- 6: gb\_pat.\*
- 7: gb\_ph.\*
- 8: gb\_pl.\*
- 9: gb\_pr.\*
- 10: gb\_ro.\*
- 11: gb\_sts.\*
- 12: gb\_sy.\*
- 13: gb\_un.\*
- 14: gb\_vi.\*
- 15: em\_ba.\*
- 16: em\_fun.\*
- 17: em\_hum.\*
- 18: em\_in.\*
- 19: em\_mu.\*

11-10-03

20: em\_om:\*  
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 22: em\_ov:\*  
 23: em\_pat:\*  
 24: em\_ph:\*  
 25: em\_pl:\*  
 26: em\_ro:\*  
 27: em\_sts:\*  
 28: em\_un:\*  
 29: em\_vi:\*  
 30: em\_htg\_hum:\*  
 31: em\_htg\_inv:\*  
 32: em\_htg\_other:\*  
 33: em\_htg\_mus:\*  
 34: em\_htg\_pln:\*  
 35: em\_htg\_rod:\*  
 36: em\_htg\_mam:\*  
 37: em\_htg\_vrt:\*  
 38: em\_sy:\*  
 39: em\_htgo\_hum:\*  
 40: em\_htgo\_mus:\*  
 41: em\_htgo\_other:\*

Pred. No. is the number of results predicted by chance to have a  
 score greater than or equal to the score of the result being printed,  
 and is derived by analysis of the total score distribution.

#### SUMMARIES

Result	% Query					Score/Length
	No.	Score	Match	Length	DB ID	
c 3	1	20	100	20	6 AR110470	1
	2	20	100	20	6 AR116450	1
		20	100	20	6 AR116461	1
	4	20	100	20	6 AX104119	1
	5	20	100	20	6 AX164692	1
	6	20	100	20	6 AX355435	1
	7	20	100	20	6 AX547172	1
	8	20	100	20	6 BD074607	1
c 9		20	100	20	6 BD074618	1
c 594		10	50	10	6 AX153495	1
c 595		10	50	10	6 AX153496	1
c8723		8	40	9	6 A94680	0.888889
c8724		8	40	9	6 AX023498	0.888889
c8725		8	40	9	6 AX668925	0.888889
c8726		8	40	9	6 AX668927	0.888889
c8727		8	40	9	6 AX668975	0.888889
324	10.4		52	12	6 AR167736	0.866667

325	10.4	52	12	6 E29620	0.866667
326	10.4	52	12	6 E38726	0.866667
327	10.4	52	12	6 E64152	0.866667
1308	9.4	47	11	6 AR301743	0.854545
c1309	9.4	47	11	6 AX623125	0.854545
c1310	9.4	47	11	6 AX627385	0.854545
c1311	9.4	47	11	6 AX630546	0.854545
1312	9.4	47	11	6 BD124493	0.854545
c 12	14.4	72	17	6 AR188734	0.847059
c5022	8.4	42	10	6 AR107817	0.84
c5023	8.4	42	10	6 AX152505	0.84
c5024	8.4	42	10	6 AX152506	0.84
5025	8.4	42	10	6 AX152507	0.84
5026	8.4	42	10	6 AX152729	0.84
c5027	8.4	42	10	6 AX153313	0.84
c5028	8.4	42	10	6 AX153314	0.84
c5029	8.4	42	10	6 AX153315	0.84
c5030	8.4	42	10	6 AX153316	0.84
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c5033	8.4	42	10	6 AX153319	0.84
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c5037	8.4	42	10	6 AX301480	0.84
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c5040	8.4	42	10	6 BD083124	0.84
c5041	8.4	42	10	6 BD161262	0.84
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c 11	14.8	74	18	6 AR190756	0.822222
17848	7.4	37	9	6 AX205250	0.822222
17849	7.4	37	9	6 AX668699	0.822222
17850	7.4	37	9	6 AX668700	0.822222
c2343	9	45	11	6 AX482038	0.818182
c2344	9	45	11	6 AX511277	0.818182
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c2346	9	45	11	6 AX625164	0.818182
c2347	9	45	11	6 AX625382	0.818182
c2348	9	45	11	6 AX629145	0.818182
c2349	9	45	11	6 AX629339	0.818182
c2350	9	45	11	6 AX631056	0.818182
c2351	9	45	11	6 AX632585	0.818182

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c 10	15	75	19	6 AX129247	0.789474
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17	13.4	67	17	6 AR174508	0.788235
c 18	13.4	67	17	6 AR186508	0.788235
c29912	7	35	9	6 AX017438	0.777778
c29913	7	35	9	6 AX538878	0.777778
c29914	7	35	9	6 AX668947	0.777778
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c29916	7	35	9	6 BD138429	0.777778
c 21	13	65	17	6 AR192172	0.764706
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c5067	8.4	42	11	6 AX629263	0.763636
c5068	8.4	42	11	6 AX629507	0.763636
5069	8.4	42	11	6 AX629798	0.763636
c5070	8.4	42	11	6 AX629883	0.763636
c5071	8.4	42	11	6 AX630156	0.763636
c5072	8.4	42	11	6 AX630273	0.763636
5073	8.4	42	11	6 AX630546	0.763636
c5074	8.4	42	11	6 AX630717	0.763636
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c 794	9.8	49	13	6 AR136587	0.753846
795	9.8	49	13	6 AR285088	0.753846
c 796	9.8	49	13	6 AR285113	0.753846
797	9.8	49	13	6 BD091222	0.753846
c 23	12.8	64	17	6 AR190307	0.752941

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: November 5, 2003, 03:17:58 ; Search time 155 Seconds  
(without alignments)  
348.315 Million cell updates/sec

Title: US-09-774-809-31  
Perfect score: 20  
Sequence: 1 gtccgggccaggccaaagtc 20

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 2100800

Minimum DB seq length: 8  
Maximum DB seq length: 30

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 65000 summaries

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 23: /SIDS1/gcgdata/geneseq/geneseqn-emb/NA2001B.DAT:\*  
 24: /SIDS1/gcgdata/geneseq/geneseqn-emb/NA2002.DAT:\*  
 25: /SIDS1/gcgdata/geneseq/geneseqn-emb/NA2003.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	% Query		Length	DB ID	Score/Length
	Score	Match			
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c 1	20	100	20	20 AAX29342	1
2	20	100	20	20 AAX29331	1
3	20	100	20	21 AAC62874	1
c 4	20	100	20	21 AAC62885	1
5	20	100	20	21 AAA48651	1
6	20	100	20	22 AAH23754	1
7	20	100	20	22 AAF99183	1
8	20	100	20	24 ABS77827	1
9	20	100	20	24 ABL39057	1
c 953	10	50	10	21 AAZ81584	1
c 954	10	50	10	21 AAZ86676	1
c 955	10	50	10	22 AAH64570	1
c 956	10	50	10	22 AAH64571	1
12341	8	40	8	21 AAA80792	1
c3487	9	45	10	21 AAZ79191	0.9
c3488	9	45	10	21 AAZ82328	0.9
3489	9	45	10	21 AAZ85483	0.9
c3490	9	45	10	21 AAZ86477	0.9
c3491	9	45	10	21 AAZ86559	0.9
c3492	9	45	10	24 ABL52193	0.9
c3493	9	45	10	24 AAS19877	0.9
3494	9	45	10	24 AAD26166	0.9
c12342	8	40	9	19 AAV63091	0.888889
c12343	8	40	9	20 AAX99683	0.888889
c12344	8	40	9	24 ABQ72076	0.888889
c12345	8	40	9	24 ABQ72078	0.888889
c12346	8	40	9	24 ABQ72126	0.888889
c43693	7	35	8	17 AAT09655	0.875
c43694	7	35	8	17 AAT09656	0.875
43695	7	35	8	17 AAT09366	0.875
43696	7	35	8	17 AAT09389	0.875
43697	7	35	8	17 AAT09459	0.875
c43698	7	35	8	17 AAT09572	0.875

c43699	7	35	8	20 AAX29560	0.875
c43700	7	35	8	20 AAX29558	0.875
43701	7	35	8	21 AAA80793	0.875
43702	7	35	8	21 AAA81046	0.875
c43703	7	35	8	22 AAD22387	0.875
444	10.4	52	12	20 AAZ41523	0.866667
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446	10.4	52	12	22 AAC97874	0.866667
10	15.4	77	18	19 AAV60744	0.855556
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c2022	9.4	47	11	21 AAF20603	0.854545
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c7217	8.4	42	10	17 AAT29327	0.84
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c7224	8.4	42	10	21 AAZ77977	0.84
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7226	8.4	42	10	21 AAZ81571	0.84
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7229	8.4	42	10	21 AAZ82634	0.84
c7230	8.4	42	10	21 AAZ82905	0.84
c7231	8.4	42	10	21 AAZ83555	0.84
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c7256	8.4	42	10	22 AAF74058	0.84
c7257	8.4	42	10	22 AAF33342	0.84
c7258	8.4	42	10	22 AAF33708	0.84
c7259	8.4	42	10	22 AAF34406	0.84
c7260	8.4	42	10	22 AAF35939	0.84
c7261	8.4	42	10	22 AAF41896	0.84
7262	8.4	42	10	22 AAF42385	0.84
c7263	8.4	42	10	22 AAF43779	0.84
7264	8.4	42	10	24 ABV84222	0.84
c7265	8.4	42	10	24 ABV84641	0.84
c7266	8.4	42	10	24 ABV84947	0.84
c7267	8.4	42	10	24 ABV78373	0.84
7268	8.4	42	10	24 ABK95837	0.84
7269	8.4	42	10	24 ABK95838	0.84
c7270	8.4	42	10	24 ABA97040	0.84
c7271	8.4	42	10	24 ABK64054	0.84
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7274	8.4	42	10	24 ABK24232	0.84
7275	8.4	42	10	24 AAS99275	0.84
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957	10	50	12	25 ABZ72939	0.833333
c 15	14	70	17	18 AAX74911	0.823529
c 13	14.8	74	18	18 AAX73494	0.822222
c26038	7.4	37	9	20 AAX54706	0.822222
c26039	7.4	37	9	21 AAF20275	0.822222
c26040	7.4	37	9	21 AAA34153	0.822222
26041	7.4	37	9	24 ABQ71850	0.822222
26042	7.4	37	9	24 ABQ71851	0.822222
c3495	9	45	11	24 ABQ81865	0.818182
c3496	9	45	11	24 ABV62890	0.818182
c3497	9	45	11	24 ABV64419	0.818182
c3498	9	45	11	24 ABV64637	0.818182
c3499	9	45	11	24 ABV68400	0.818182
c3500	9	45	11	24 ABV68594	0.818182
c3501	9	45	11	24 ABV70311	0.818182
c3502	9	45	11	24 ABV71840	0.818182
c12347	8	40	10	14 AAQ51821	0.8
12348	8	40	10	16 AAQ96792	0.8

12349	8	40	10	16 AAQ96793	0.8
c12350	8	40	10	16 AAQ88580	0.8
c12351	8	40	10	20 AAX54584	0.8
c12352	8	40	10	20 AAX18625	0.8
c12353	8	40	10	21 AAF20153	0.8
12354	8	40	10	21 AAC73935	0.8
c12355	8	40	10	21 AAA56555	0.8
c12356	8	40	10	21 AAA34031	0.8
c12357	8	40	10	21 AAZ77634	0.8
c12358	8	40	10	21 AAZ79103	0.8
c12359	8	40	10	21 AAZ79322	0.8
c12360	8	40	10	21 AAZ81594	0.8
12361	8	40	10	21 AAZ82082	0.8
12362	8	40	10	21 AAZ83064	0.8
c12363	8	40	10	21 AAZ83312	0.8
c12364	8	40	10	21 AAZ83787	0.8
12365	8	40	10	21 AAZ83855	0.8
12366	8	40	10	21 AAZ83864	0.8
12367	8	40	10	21 AAZ84284	0.8
c12368	8	40	10	21 AAZ85316	0.8
c12369	8	40	10	21 AAZ85453	0.8
c12370	8	40	10	21 AAZ85585	0.8
c12371	8	40	10	21 AAZ85596	0.8
12372	8	40	10	21 AAZ85958	0.8
12373	8	40	10	22 ABA06090	0.8
12374	8	40	10	22 ABA06204	0.8
12375	8	40	10	22 AAH63781	0.8
c12376	8	40	10	22 AAH64036	0.8
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c12378	8	40	10	22 AAH64374	0.8
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12380	8	40	10	22 AAH64388	0.8
12381	8	40	10	22 AAH64389	0.8
12382	8	40	10	22 AAH64390	0.8
12383	8	40	10	22 AAH64391	0.8
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12385	8	40	10	22 AAH64393	0.8
12386	8	40	10	22 AAH64394	0.8
12387	8	40	10	22 AAH32825	0.8
c12388	8	40	10	22 AAH32856	0.8
c12389	8	40	10	22 AAF39487	0.8
c12390	8	40	10	22 AAF41493	0.8
12391	8	40	10	24 ABV84307	0.8
12392	8	40	10	24 ABV84789	0.8
12393	8	40	10	24 ABV84947	0.8
12394	8	40	10	24 ABV78373	0.8
12395	8	40	10	24 ABV78459	0.8
12396	8	40	10	24 ABL57664	0.8
12397	8	40	10	24 ABK95840	0.8

c12398	8	40	10	24 ABK72637	0.8
c12399	8	40	10	24 ABK17015	0.8
12400	8	40	10	24 AAS99416	0.8
12401	8	40	10	24 AAS95685	0.8
12402	8	40	10	24 ABL36370	0.8
12403	8	40	10	24 ABL42671	0.8
12404	8	40	10	24 ABL42760	0.8
c12405	8	40	10	24 ABL42855	0.8
c 11	15	75	19	21 AAA82879	0.789474
c 12	15	75	19	22 AAH58041	0.789474
c 21	13.4	67	17	18 AAX69246	0.788235
22	13.4	67	17	22 AAD03853	0.788235
23	13.4	67	17	24 AAS18424	0.788235
24	13.4	67	17	25 ABX16354	0.788235
c2028	9.4	47	12	20 AAX55033	0.783333
c2029	9.4	47	12	21 AAF20602	0.783333
c2030	9.4	47	12	21 AAA34480	0.783333
c43704	7	35	9	21 AAF20849	0.777778
c43705	7	35	9	21 AAA34727	0.777778
c43706	7	35	9	24 ABQ72098	0.777778
c43707	7	35	9	24 ABQ72099	0.777778
c 283	10.8	54	14	18 AAT76461	0.771429
c 284	10.8	54	14	20 AAX54253	0.771429
c 285	10.8	54	14	21 AAF19819	0.771429
c 286	10.8	54	14	21 AAA33697	0.771429
c 29	13	65	17	18 AAX74910	0.764706
7278	8.4	42	11	20 AAX54916	0.763636
7279	8.4	42	11	21 AAF20485	0.763636
7280	8.4	42	11	21 AAA34363	0.763636
c7281	8.4	42	11	21 AAZ59919	0.763636
7282	8.4	42	11	24 ABQ81854	0.763636
7283	8.4	42	11	24 ABV62380	0.763636
c7284	8.4	42	11	24 ABV62551	0.763636
7285	8.4	42	11	24 ABV62704	0.763636
7286	8.4	42	11	24 ABV63037	0.763636
7287	8.4	42	11	24 ABV65097	0.763636
7288	8.4	42	11	24 ABV65146	0.763636
c7289	8.4	42	11	24 ABV65638	0.763636
7290	8.4	42	11	24 ABV65978	0.763636
c7291	8.4	42	11	24 ABV66142	0.763636
c7292	8.4	42	11	24 ABV66964	0.763636
c7293	8.4	42	11	24 ABV67427	0.763636
7294	8.4	42	11	24 ABV67547	0.763636
c7295	8.4	42	11	24 ABV68518	0.763636
c7296	8.4	42	11	24 ABV68762	0.763636
7297	8.4	42	11	24 ABV69053	0.763636
c7298	8.4	42	11	24 ABV69138	0.763636
c7299	8.4	42	11	24 ABV69411	0.763636
c7300	8.4	42	11	24 ABV69528	0.763636

7301	8.4	42	11	24	ABV69801	0.763636
c7302	8.4	42	11	24	ABV69972	0.763636
7303	8.4	42	11	24	ABV70125	0.763636
7304	8.4	42	11	24	ABV70458	0.763636
7305	8.4	42	11	24	ABQ86459	0.763636
c7306	8.4	42	11	24	ABQ86573	0.763636
7307	8.4	42	11	24	ABQ87161	0.763636
7308	8.4	42	11	24	ABQ87207	0.763636
7309	8.4	42	11	24	ABL92021	0.763636
7310	8.4	42	11	25	ABX71946	0.763636
152	11.4	57	15	24	AAS19798	0.76
c1241	9.8	49	13	20	AAV63772	0.753846
c1242	9.8	49	13	21	AAA04950	0.753846
c1243	9.8	49	13	21	AAA05213	0.753846
c1244	9.8	49	13	23	ABC48592	0.753846
1245	9.8	49	13	23	ABC48593	0.753846
c 31	12.8	64	17	18	AAX73045	0.752941

OM nucleic - nucleic search, using sw model

Run on: November 5, 2003, 06:43:01 ; Search time 52 Seconds  
(without alignments)  
169.763 Million cell updates/sec

Title: US-09-774-809-31  
Perfect score: 20  
Sequence: 1 gtccgggccaggccaaagtc 20

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 544510

Minimum DB seq length: 8  
Maximum DB seq length: 30

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 65000 summaries

Database : Issued\_Patents\_NA:\*  
1: /cgn2\_6/ptodata/2/ina/5A\_COMB.seq:\*  
2: /cgn2\_6/ptodata/2/ina/5B\_COMB.seq:\*  
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5: /cgn2\_6/ptodata/2/ina/PCTUS\_COMB.seq:\*  
6: /cgn2\_6/ptodata/2/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Query		Length	DB ID	Score/Length
	Score	% Match			
c 2	1 20	100	20	2 US-08-910-629A-31	1
	2 20	100	20	2 US-08-910-629A-42	1
	3 20	100	20	3 US-09-209-668-7	1

4	20	100	20	3 US-09-287-796-31	1
c 5	20	100	20	3 US-09-287-796-42	1
6	20	100	20	3 US-09-130-616-31	1
c 7	20	100	20	3 US-09-130-616-42	1
4597	8	40	8	3 US-08-859-954-105	1
c 8	15.4	77	17	4 US-09-371-772B-6740	0.905882
16171	7	35	8	1 US-08-105-483-423	0.875
16172	7	35	8	1 US-08-709-209-423	0.875
16173	7	35	8	1 US-08-303-275-131	0.875
16174	7	35	8	1 US-08-458-101-423	0.875
16175	7	35	8	3 US-08-859-954-106	0.875
16176	7	35	8	3 US-08-859-954-359	0.875
c 172	10.4	52	12	3 US-08-822-586-49	0.866667
173	10.4	52	12	3 US-09-281-418-100	0.866667
9	15.4	77	18	3 US-08-951-923-51	0.855556
648	9.4	47	11	4 US-09-249-155A-324	0.854545
c 12	14.4	72	17	4 US-08-584-040-4222	0.847059
c 13	14.4	72	17	4 US-09-371-772B-1989	0.847059
2575	8.4	42	10	3 US-08-388-353-387	0.84
2576	8.4	42	10	3 US-08-488-551B-387	0.84
c2577	8.4	42	10	3 US-08-522-384-63	0.84
2578	8.4	42	10	4 US-09-720-201A-24	0.84
c 18	13.4	67	16	4 US-09-371-772B-5851	0.8375
c 14	14	70	17	4 US-08-584-040-7661	0.823529
c 15	14	70	17	4 US-09-371-772B-3450	0.823529
c 10	14.8	74	18	4 US-08-584-040-6244	0.822222
c 11	14.8	74	18	4 US-09-371-772B-3004	0.822222
c 16	13.8	69	17	4 US-09-371-772B-4833	0.811765
c4598	8	40	10	2 US-08-441-887A-183	0.8
c4599	8	40	10	2 US-08-192-942-6	0.8
4600	8	40	10	3 US-08-388-353-388	0.8
4601	8	40	10	3 US-08-388-353-389	0.8
4602	8	40	10	3 US-08-488-551B-388	0.8
4603	8	40	10	3 US-08-488-551B-389	0.8
c31171	6.4	32	8	3 US-08-474-700B-43	0.8
31172	6.4	32	8	3 US-08-859-954-56	0.8
31173	6.4	32	8	3 US-08-859-954-107	0.8
c31174	6.4	32	8	3 US-09-041-675-9	0.8
31175	6.4	32	8	3 US-09-041-675-15	0.8
31176	6.4	32	8	3 US-09-041-675-23	0.8
31177	6.4	32	8	3 US-08-646-301A-10	0.8
c31178	6.4	32	8	3 US-08-646-301A-10	0.8
c31179	6.4	32	8	3 US-09-398-499-16	0.8
31180	6.4	32	8	3 US-09-398-499-39	0.8
19	13.4	67	17	3 US-08-924-183-6	0.788235
20	13.4	67	17	4 US-09-488-364-6	0.788235
c 21	13.4	67	17	4 US-08-584-040-1996	0.788235
c 22	13.4	67	17	4 US-09-371-772B-541	0.788235
c 23	13.4	67	17	4 US-09-371-772B-4834	0.788235

c 24	13	65	17	4 US-08-584-040-7660	0.764706
c 25	13	65	17	4 US-09-371-772B-3449	0.764706
c 363	9.8	49	13	3 US-08-882-046-77	0.753846
364	9.8	49	13	4 US-09-922-445-11	0.753846
c 365	9.8	49	13	4 US-09-922-445-36	0.753846
c 26	12.8	64	17	4 US-08-584-040-5795	0.752941
c 27	12.8	64	17	4 US-09-371-772B-2661	0.752941
c50444	6	30	8	1 US-07-949-541A-34	0.75
c50445	6	30	8	1 US-07-949-541A-39	0.75
c50446	6	30	8	2 US-08-593-345B-13	0.75
c50447	6	30	8	3 US-08-859-954-53	0.75
c50448	6	30	8	3 US-08-859-954-81	0.75
50449	6	30	8	3 US-08-859-954-104	0.75
c50450	6	30	8	3 US-08-859-954-329	0.75
50451	6	30	8	3 US-08-859-954-332	0.75
c50452	6	30	8	3 US-08-859-954-333	0.75
50453	6	30	8	3 US-08-859-954-360	0.75
50454	6	30	8	3 US-08-859-954-396	0.75

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: November 5, 2003, 07:13:11 ; Search time 138 Seconds  
(without alignments)  
394.173 Million cell updates/sec

Title: US-09-774-809-31  
Perfect score: 20  
Sequence: 1 gtccgggccaggccaaagtc 20

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1811591 seqs, 1359896290 residues

Total number of hits satisfying chosen parameters: 926388

Minimum DB seq length: 8  
Maximum DB seq length: 30

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 65000 summaries

Database : Published\_Applications\_NA:\*

- 1: /cgn2\_6/ptodata/1/pubpna/US07\_PUBCOMB.seq:\*
- 2: /cgn2\_6/ptodata/1/pubpna/PCT\_NEW\_PUB.seq:\*
- 3: /cgn2\_6/ptodata/1/pubpna/US06\_NEW\_PUB.seq:\*
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- 5: /cgn2\_6/ptodata/1/pubpna/US07\_NEW\_PUB.seq:\*
- 6: /cgn2\_6/ptodata/1/pubpna/PCTUS\_PUBCOMB.seq:\*
- 7: /cgn2\_6/ptodata/1/pubpna/US08\_NEW\_PUB.seq:\*
- 8: /cgn2\_6/ptodata/1/pubpna/US08\_PUBCOMB.seq:\*
- 9: /cgn2\_6/ptodata/1/pubpna/US09A\_PUBCOMB.seq:\*
- 10: /cgn2\_6/ptodata/1/pubpna/US09B\_PUBCOMB.seq:\*
- 11: /cgn2\_6/ptodata/1/pubpna/US09C\_PUBCOMB.seq:\*
- 12: /cgn2\_6/ptodata/1/pubpna/US09\_NEW\_PUB.seq:\*
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- 14: /cgn2\_6/ptodata/1/pubpna/US10B\_PUBCOMB.seq:\*
- 15: /cgn2\_6/ptodata/1/pubpna/US10\_NEW\_PUB.seq:\*
- 16: /cgn2\_6/ptodata/1/pubpna/US60\_NEW\_PUB.seq:\*
- 17: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

Result	% Query		Length	DB	ID	Score/Length
	No.	Score Match				
	1	20	100	20	11 US-09-774-809-31	1
c 2		20	100	20	11 US-09-774-809-42	1
	3	20	100	20	11 US-09-888-326-463	1
	4	20	100	20	11 US-09-776-479-311	1
	5	20	100	20	14 US-10-112-653-301	1
	6	20	100	20	14 US-10-017-995-311	1
c 565		10	50	10	12 US-10-330-627-1410	1
c 566		10	50	10	12 US-10-330-627-1411	1
c2292		9	45	10	13 US-10-033-145-1619	0.9
c8456		8	40	9	9 US-09-989-789-2374	0.888889
c8457		8	40	9	9 US-09-989-789-2376	0.888889
c8458		8	40	9	9 US-09-989-789-2424	0.888889
c8459		8	40	9	11 US-09-990-186-2374	0.888889
c8460		8	40	9	11 US-09-990-186-2376	0.888889
c8461		8	40	9	11 US-09-990-186-2424	0.888889
c8462		8	40	9	11 US-09-989-994-2374	0.888889
c8463		8	40	9	11 US-09-989-994-2376	0.888889
c8464		8	40	9	11 US-09-989-994-2424	0.888889
c32015		7	35	8	10 US-09-837-751-13	0.875
7		17	85	20	14 US-10-007-010-56	0.85
c5017		8.4	42	10	12 US-10-329-465-204	0.84
c5018		8.4	42	10	12 US-10-330-627-420	0.84
c5019		8.4	42	10	12 US-10-330-627-421	0.84
5020		8.4	42	10	12 US-10-330-627-422	0.84
5021		8.4	42	10	12 US-10-330-627-644	0.84
c5022		8.4	42	10	12 US-10-330-627-1228	0.84
c5023		8.4	42	10	12 US-10-330-627-1229	0.84
c5024		8.4	42	10	12 US-10-330-627-1230	0.84
c5025		8.4	42	10	12 US-10-330-627-1231	0.84
c5026		8.4	42	10	12 US-10-330-627-1232	0.84
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c5029		8.4	42	10	13 US-10-033-145-405	0.84
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567		10	50	12	10 US-09-263-959-437	0.833333
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18648		7.4	37	9	9 US-09-989-789-2149	0.822222
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18651		7.4	37	9	11 US-09-989-994-2148	0.822222
18652		7.4	37	9	11 US-09-989-994-2149	0.822222

18653	7.4	37	9	12 US-10-277-494-167	0.822222
c2293	9	45	11	12 US-10-055-728-15	0.818182
8465	8	40	10	12 US-10-330-627-621	0.8
c8466	8	40	10	12 US-10-330-627-876	0.8
c8467	8	40	10	12 US-10-330-627-877	0.8
c8468	8	40	10	12 US-10-330-627-1214	0.8
c8469	8	40	10	12 US-10-330-627-1215	0.8
8470	8	40	10	12 US-10-330-627-1228	0.8
8471	8	40	10	12 US-10-330-627-1229	0.8
8472	8	40	10	12 US-10-330-627-1230	0.8
8473	8	40	10	12 US-10-330-627-1231	0.8
8474	8	40	10	12 US-10-330-627-1232	0.8
8475	8	40	10	12 US-10-330-627-1233	0.8
8476	8	40	10	12 US-10-330-627-1234	0.8
c8477	8	40	10	12 US-10-438-683-6	0.8
c8478	8	40	10	13 US-10-033-145-62	0.8
c8479	8	40	10	13 US-10-033-145-1531	0.8
c8480	8	40	10	13 US-10-033-145-1750	0.8
60658	6.4	32	8	13 US-10-027-632-176277	0.8
9	13.4	67	17	13 US-10-020-038-6	0.788235
c32016	7	35	9	9 US-09-989-789-2396	0.777778
c32017	7	35	9	9 US-09-989-789-2397	0.777778
c32018	7	35	9	11 US-09-990-186-2396	0.777778
c32019	7	35	9	11 US-09-990-186-2397	0.777778
c32020	7	35	9	11 US-09-989-994-2396	0.777778
c32021	7	35	9	11 US-09-989-994-2397	0.777778
5031	8.4	42	11	12 US-10-055-728-4	0.763636
842	9.8	49	13	13 US-10-005-212-7	0.753846

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OM nucleic - nucleic search, using sw model

Run on: November 5, 2003, 03:43:24 ; Search time 1279 Seconds  
(without alignments)  
380.054 Million cell updates/sec

Title: US-09-774-809-31  
Perfect score: 20  
Sequence: 1 gtccgggccaggccaaagtc 20

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 33250

Minimum DB seq length: 8  
Maximum DB seq length: 30

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 65000 summaries

Database : EST:\*  
1: em\_estba:\*  
2: em\_esthum:\*  
3: em\_estin:\*  
4: em\_estmu:\*  
5: em\_estov:\*  
6: em\_estpl:\*  
7: em\_estro:\*  
8: em\_htc:\*  
9: gb\_est1:\*  
10: gb\_est2:\*  
11: gb\_htc:\*  
12: gb\_est3:\*  
13: gb\_est4:\*  
14: gb\_est5:\*  
15: em\_estfun:\*  
16: em\_estom:\*  
17: em\_gss\_hum:\*  
18: em\_gss\_inv:\*  
19: em\_gss\_pln:\*

20: em\_gss\_vrt:\*  
 21: em\_gss\_fun:\*  
 22: em\_gss\_mam:\*  
 23: em\_gss\_mus:\*  
 24: em\_gss\_pro:\*  
 25: em\_gss\_rod:\*  
 26: em\_gss\_phg:\*  
 27: em\_gss\_vrl:\*  
 28: gb\_gss1:\*  
 29: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a  
 score greater than or equal to the score of the result being printed,  
 and is derived by analysis of the total score distribution.

#### SUMMARIES

Result		%				
No.	Score	Match	Length	DB	ID	Score/Length
c2824	6	30	8	14	CD486474	0.75